AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on line 19 of page 2 to read as follows:

Representative of the sacromastigophoric protozoa that are able to evade immune systems is *Trypanosoma brucei*. *Trypanosoma brucei* is a pathological organism that has the ability to evade human immune system surveillance, specifically infect cells that display a receptor for gp83 trans-sialidase (gp83-TSA) expressed on the surface of Trypanosomes, and a natural ability to transfer genetic information to its host. *Trypanosome brucei* evades the immune system by continually changing its surface coat, can live in the bloodstream for an indefinite period of time, and has an unlimited capacity for carrying genetic material. These characteristics are attractive for developing the Trypanosome organism into an allogous cell-based protein delivery system. Trypanosomatids have a digenetic life cycle that involves mammalian and insect hosts and are responsible for a variety of diseases in humans and domestics animals. The Trypanosoma genus contains three human and a number of animal pathogens. The Central and South American *Trypanosoma cruzi* is an intercellular parasite responsible for Chagas' disease. *Trypanosoma brucei* subspecies *rhodesiense* and *gambiense* are the causative agents of sleeping sickness. *Trypanosoma brucei brucei* causes Nagana, a wasting disease in domestic animals. The *T. brucei brucei* strain, which is not pathogenic for humans, can live in the bloodstream. While in the mammalian bloodstream *T. brucei brucei* is protected from the immune system by a variable surface glycoprotein (VSG) coat. This organism is morphologically and biochemically similar to the other two *T. brucei* subspecies but is sensitive to a non-immune factor in human serum called haptoglobin-related protein ~~(Hrp)~~ <u>(Hpr)</u>.

Please amend the paragraph beginning on line 17 of page 6 to read as follows:

Figure 1 is a schematic representation of a regulated tetracycline inducible expression construct operative in an inventive delivery system;

Figure 2 shows amplification of VP1-4 capsid genes from the RNA genome of EV1 using RT-PCR;

Figure 3 shows PCR duplication of T7lac and p10 promoters from pTriEx-1.1;

Figure 4 shows a comparison of duplicated composite promoters (SEQ ID Nos. 31-34);

Figure 5 shows native (SEQ ID No. 21) and recombinant (SEQ ID No. 20) VP1 gene DNA sequence comparison;

Figure 6 shows native (SEQ ID No. 23) and recombinant (SEQ ID No. 22) VP2 gene DNA sequence comparison;

Figure 7 shows native (SEQ ID No. 25) and recombinant (SEQ ID No. 24) VP3 gene DNA sequence comparison;

Figure 8 shows native (SEQ ID No. 27) and recombinant (SEQ ID No. 26) VP4 gene DNA sequence comparison;

Figure 9 is a diagram of pLCRC, a multiple gene expression vector for use in trypanosome;

Figure 10 is a diagram of a haptoglobin-related protein construct (SEQ ID No. 30) showing coding sequence as the N-terminal antibody tag and a bipartite C-terminal sequence for targeting to a lysosome; and

Figure 11 is a DNA (SEQ ID No. 28) and amino acid (SEQ ID No. 29) sequence for haptoglobin related protein showing the codons, gene and single nucleotide polymorphisms.

Please amend the paragraph beginning on line 11 of page 11 to read as follows:

The mode of administration according to the present invention is dictated by convenience and survival of at least a portion of the administered population of sacromastigophoric organisms. Preferably, an organism according to the present invention is delivered ~~parentally~~ parenterally. More preferably, the inventive organism is delivered by intravenous parenteral injection. It is appreciated that other routes of administration are also operative herein, these alternate routes illustratively including intracisternally, intrathecally, intravaginally, intraperitoneally, intravesically, or as a buccal or nasal spray.

Please amend the paragraph beginning on line 3 of page 29 to read as follows:

The smallest capsid gene, VP4, was cloned first using EcoRV and BglII to produce pLCVP4. The VP4 structural (VP4s) gene was cloned using RT-PCR. TP13 (SEQ ID NO. 13) and TP14 (SEQ ID NO. 14) are the primers and the EV1 RNA genome is the template. The VP4s contains a unique Eco RI restriction site that was maintained. By keeping the native Eco RI restriction site a serine residue is added onto the carboxyl terminal of the VP4 protein. The original T7/lac and p10 operators present in the pTriEx-1.1 vector drive VP4 gene expression. VP4 is a unique opportunity because of the possibility of forming chimeric molecules with the target protein in the carboxyl terminal half of VP4. This helps in subcloning because it eliminates the necessary removal of target gene stop codons and thus creates an opportunity for the insertion of multiple target genes simultaneously. A unique Avr I restriction site was introduced into the VP4s to allow for creating chimeric molecules with a linker region that starts at $VP4_{51}$. The Avr I restriction site modifies the native VP4s sequence by introducing silent mutations. The silent mutations alter the native nucleic acid sequence ~~(CCT GGT) to (CCC GGG)~~ but will not change the protein composition ~~(Pro-Gly)~~. The recombinant VP4s was cloned

into the pTriEx-1.1 vector using the Eco RV and Bgl II unique restriction sites. By cloning into the Eco RV restriction site we pick up the initiator methionine (M), alanine (A) and serine (S). This will mutate the native VP4 amino terminal sequence MGAQ to MAIS. The VP4s cloning task was completed by DNA sequencing to insure proper nucleotide incorporation and that the gene was cloned in frame with the initial ATG translation start sequence as shown in Figure 8. The VP4s encodes for a protein with a predicted molecular weight of 6800 Da.